

679872SequenceListingThirdSubstitutetxt.txt
SEQUENCE LISTING

<110> Desire, Laurent

<120> BACE455, AN ALTERNATIVE SPLICE VARIANT OF THE HUMAN
BETA-SECRETASE

<130> 67987.000002

<140> 10/578,493

<141> 2006-05-05

<150> PCT/IB2004/003897

<151> 2004-11-05

<150> 60/517,401

<151> 2003-11-03

<160> 36

<170> PatentIn version 3.5

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<212> DNA

<213> Homo sapiens

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	gtgggcagcc cccgcagac gctcaacatc ctggtgata caggcagcag taactttgca	300
	gtgggtgctg ccccccaccc cttccctgcat cgctactacc agaggcagct gtccagcaca	360
	taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag	420
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	attgtggaca gtggcaccac caacccctgt ttgcccaaga aagtgtttga agctgcagtc	780
	aaatccatca aggcagcctc ctccacggag aagttccctg atggttctg gctaggagag	840
	cagctggtgt gctggcaagc aggcaccacc ctttggaaaca tttcccagt catctcactc	900
	tacctaattgg gtgaggatcc caaccagtcc ttccgcatca ccatccttcc gcagcaatac	960
	ctgcggccag tggaagatgt ggcacgtcc caagacgact gttacaagtt tgccatctca	1020
	cagtcatcca cggcactgt tatggagct gttatcatgg agggcttcta cggtgtcttt	1080

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gccctttca	tgctgccact	ctgcctcatg	gtgtgtcagt	ggcgctgcct	ccgctgcctg	1320
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Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
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Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro-Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

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Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Ile Ile Gly
180 185 190

Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
195 200 205

Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
210 215 220

Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
225 230 235 240

Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
245 250 255

Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
260 265 270

Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
275 280 285

Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
290 295 300

Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
305 310 315 320

Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
325 330 335

Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
340 345 350

Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
355 360 365

Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
370 375 380

Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
385 390 395 400

Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met
405 410 415

Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys
420 425 430

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Asp Asp Ile Ser Leu Leu Lys
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<210> 3
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<212> PRT
<213> Artificial Sequence

<220>
<223> Distinctive fragment of a BACE455 polypeptide

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Ile Ala Arg Ile Ile Gly
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<210> 4
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Distinctive fragment of a BACE455 polypeptide

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Glu Ile Ala Arg Ile Ile Gly
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<210> 5
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<212> PRT
<213> Artificial Sequence

<220>
<223> Distinctive fragment of a BACE455 polypeptide

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Glu Ile Ala Arg Ile Ile Gly Gly
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<210> 6
<211> 8
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<213> Artificial Sequence

<220>
<223> Distinctive fragment of a BACE455 polypeptide

<400> 6

Ala Glu Ile Ala Arg Ile Ile Gly
1 5

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<210> 7
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> Distinctive fragment of a BACE455 polypeptide

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Ala Glu Ile Ala Arg Ile Ile Gly Gly
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<210> 8
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Distinctive fragment of a BACE455 polypeptide

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Ala Glu Ile Ala Arg Ile Ile Gly Gly Ile
1 5 10

<210> 9
<211> 9
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<220>
<223> Distinctive fragment of a BACE455 polypeptide

<400> 9

Tyr Ala Glu Ile Ala Arg Ile Ile Gly
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<210> 10
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<213> Artificial sequence

<220>
<223> Distinctive fragment of a BACE455 polypeptide

<400> 10

Tyr Ala Glu Ile Ala Arg Ile Ile Gly Gly
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<210> 11
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679872SequenceListingThirdSubstitutetxt.txt

<220>
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<400> 11

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<223> probe

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18

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gggctggcct

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atgctgagat

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<210> 16
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<223> primer

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<210> 17
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<220>
<223> primer

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gatcat

6

<210> 18
<211> 10
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<400> 18
tggaggtatc

10

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<400> 19
gaccactcg

10

<210> 20
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<212> DNA
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<223> primer

<400> 20
tgtacacagg

10

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cagtctctgg

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<210> 22
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<223> primer

<400> 22
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6

<210> 23
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<220>
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<400> 23
ccaggatc

8

<210> 24
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<220>
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<400> 24
gccaggatca

10

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<220>
<223> primer

<400> 25
attgccagga tcattgga

18

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<400> 26
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21

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<223> primer

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<210> 28
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<400> 28
cccgcagacg ctcaacatc

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<210> 29
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<210> 31
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<223> primer

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679872SequenceListingThirdSubstitutetxt.txt

<213> Artificial Sequence

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<223> fluorogenic App-based peptide MCA

<400> 32

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<211> 8

<212> PRT

<213> Homo sapiens

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Leu Val Asn Met Ala Glu Gly Asp
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<210> 36

<211> 501

<212> PRT

<213> Homo sapiens

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679872SequenceListingThirdSubstitutetxt.txt

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Cys Ala Gly Phe Pro Leu Asn Gln
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
245 250 255

679872SequenceListingThirdSubstitutetxt.txt

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
435 440 445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
450 455 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
465 470 475 480

Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
485 490 495

Ile Ser Leu Leu Lys
500